

SEQUENCE LISTING

<110> AUBURN UNIVERSITY
UNIVERSITY OF CENTRAL FLORIDA

<120> PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS

<130> 1463-PCT-00

<140> 09/807,721

<141> 2001-04-18

<150> PCT/US01/06274

<151> 2001-02-28

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 2059

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (17..1381, 1409..2050)

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ctg	gtg	aaa	cct	ggg	gcc	tca	gtg	aag	ata	tcc	tgc	aag	gct	tct	gga	97
Leu	Val	Lys	Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	
	15				20							25				

tac	aca	ttc	act	gac	tac	aac	ata	cac	tgg	gtg	aag	cag	agc	cgt	gga	145
Tyr	Thr	Phe	Thr	Asp	Tyr	Asn	Ile	His	Trp	Val	Lys	Gln	Ser	Arg	Gly	
	30					35					40					

aag	agc	ctt	gag	tgg	att	gga	tat	att	tat	cct	tac	aat	ggt	aat	act	193
Lys	Ser	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Gly	Asn	Thr	
	45				50					55						

tac	tac	aac	cag	aag	ttc	aag	aac	aag	gcc	aca	ttg	act	gta	gac	aat	241
Tyr	Tyr	Asn	Gln	Lys	Phe	Lys	Asn	Lys	Ala	Thr	Leu	Thr	Val	Asp	Asn	
	60				65				70					75		

tcc	tcc	acc	tca	gcc	tac	atg	gag	ctc	cgc	agc	ctg	aca	tct	gag	gac	289
Ser	Ser	Thr	Ser	Ala	Tyr	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	
			80					85						90		

tct	gca	gtc	tat	tac	tgt	gca	acc	tac	ttt	gac	tac	tgg	ggc	caa	ggc	337
Ser	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	
			95					100					105			

acc act ctc aca gtg agc tca gaa tcc ccg acc agc ccc aag gtc ttc	385
Thr Thr Leu Thr Val Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe	
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ccg ctg agc ctc gac agc acc ccc caa gat ggg aac gtg gtc gtc gca	433
Pro Leu Ser Leu Asp Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala	
125 130 135	
tgc ctg gtc cag ggc ttc ttc ccc cag gag cca ctc agt gtg acc tgg	481
Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp	
140 145 150 155	
agc gaa agc gga cag aac gtg acc gcc aga aac ttc cca cct agc cag	529
Ser Glu Ser Gly Gln Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln	
160 165 170	
gat gcc tcc ggg gac ctg tac acc acg agc agc cag ctg acc ctg ccg	577
Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu Pro	
175 180 185	
gcc aca cag tgc cca gac ggc aag tcc gtg aca tgc cac gtg aag cac	625
Ala Thr Gln Cys Pro Asp Gly Lys Ser Val Thr Cys His Val Lys His	
190 195 200	
tac acg aat tcc agc cag gat gtg act gtg ccc tgc cga gtt ccc cca	673
Tyr Thr Asn Ser Ser Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro	
205 210 215	
cct ccc cca tgc tgc cac ccc cga ctg tgc ctg ccc cga ccg gcc ctc	721
Pro Pro Pro Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu	
220 225 230 235	
gag gac ctg ctg tta ggt tca gaa gcg aac ctc acg tgc aca ctg acc	769
Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr	
240 245 250	
ggc ctg aga gat gcc tct ggt gcc acc ttc acc tgg acg ccc tca agt	817
Gly Leu Arg Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser	
255 260 265	
ggg aag agc gct gtt caa gga cca cct gag cgt gac ctc tgt ggc tgc	865
Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys	
270 275 280	
tac agc gtg tca tca gta ctt cct gcc tgt gcc cag cca tgg aac cat	913
Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His	
285 290 295	
ggg gag acc ttc acc tgc act gct gcc cac ccc gag ttg aag acc cca	961
Gly Glu Thr Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro	
300 305 310 315	
cta acc gcc aac atc aca aaa tcc gga aac aca ttc cgg ccc gag gtc	1009
Leu Thr Ala Asn Ile Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val	
320 325 330	
cac ctg ctg ccg ccg ccg tgc gag gag ctg gcc ctg aac gag ctg gtg	1057

His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val
 335 340 345
 acg ctg acg tgc ctg gca cgt ggc ttc agc ccc aag gat gtg ctg gtt 1105
 Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val
 350 355 360
 cgc tgg ctg cag ggg tca cag gag ctg ccc cgc gag aag tac ctg act 1153
 Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr
 365 370 375
 tgg gca tcc cgg cag gag ccc agc cag ggc acc acc acc tat gct gtg 1201
 Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Tyr Ala Val
 380 385 390 395
 acc agc ata ctg cgc gtg gca gcc gag gac tgg aag aag ggg gag acc 1249
 Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr
 400 405 410
 ttc tcc tgc atg gtg ggc cac gag gcc ctg ccg ctg gcc ttc aca cag 1297
 Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln
 415 420 425
 aag acc atc gac cgc ttg gcg ggt aaa ccc acc cat atc aat gtg tct 1345
 Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser
 430 435 440
 gtt gtc atg gog gag gcg gac ggc acc tgc tac aga tgaaatattg 1391
 Val Val Met Ala Glu Ala Asp Gly Thr Cys Tyr Arg
 445 450 455
 cggatccgga gggattt atg gac att gtg atg acc cag tct cca gca atc 1441
 Met Asp Ile Val Met Thr Gln Ser Pro Ala Ile
 460 465
 atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc 1489
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
 470 475 480
 tca atg gta agt tac atg cac tgg ttc cag cag aag cca ggc act tct 1537
 Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser
 485 490 495
 ccc aaa ctg tgg ctt tat agc aca tcc aac ctg gct tct gga gtc cct 1585
 Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
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 gct cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctg aca atc 1633
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 515 520 525 530
 agc cga atg gag gct gaa gat gct gcc act tat tac tgc cat caa agg 1681
 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg
 535 540 545
 act agc tac cca tac aca ttc gga ggg ggg acc aag ctt gag atc aaa 1729
 Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

550

555

560

cga act gtg ggt gca cca tct gtc ttc atc ttc ccg cca tct gat gag 1777
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 565 570 575

cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 1825
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 580 585 590

tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctg caa 1873
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 595 600 605 610

tgg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 1921
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 615 620 625

acc tac agc ctg agc agc acc ctg acg ctg agc aaa gca gac tac gag 1969
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 630 635 640

aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag gcc ctg agc tgg 2017
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
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<210> 2

<211> 669

<212> PRT

<213> Homo sapiens

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Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu Glu Trp
 35 40 45

Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn Gln Lys
 50 55 60

Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr Ser Ala
 65 70 75 80

Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
 85 90 95

Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
 100 105 110

Ser	Ser	Ala	Ser	Pro	Thr	Ser	Pro	Lys	Val	Phe	Pro	Leu	Ser	Leu	Asp	115	120	125	
Ser	Thr	Pro	Gln	Asp	Gly	Asn	Val	Val	Val	Ala	Cys	Leu	Val	Gln	Gly	130	135	140	
Phe	Phe	Pro	Gln	Glu	Pro	Leu	Ser	Val	Thr	Trp	Ser	Glu	Ser	Gly	Gln	145	150	155	160
Asn	Val	Thr	Ala	Arg	Asn	Phe	Pro	Pro	Ser	Gln	Asp	Ala	Ser	Gly	Asp	165	170	175	
Leu	Tyr	Thr	Thr	Ser	Ser	Gln	Leu	Thr	Leu	Pro	Ala	Thr	Gln	Cys	Pro	180	185	190	
Asp	Gly	Lys	Ser	Val	Thr	Cys	His	Val	Lys	His	Tyr	Thr	Asn	Ser	Ser	195	200	205	
Gln	Asp	Val	Thr	Val	Pro	Cys	Arg	Val	Pro	Pro	Pro	Pro	Pro	Cys	Cys	210	215	220	
His	Pro	Arg	Leu	Ser	Leu	His	Arg	Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu	225	230	235	240
Gly	Ser	Glu	Ala	Asn	Leu	Thr	Cys	Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala	245	250	255	
Ser	Gly	Ala	Thr	Phe	Thr	Trp	Thr	Pro	Ser	Ser	Gly	Lys	Ser	Ala	Val	260	265	270	
Gln	Gly	Pro	Pro	Glu	Arg	Asp	Leu	Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	275	280	285	
Val	Leu	Pro	Gly	Cys	Ala	Gln	Pro	Trp	Asn	His	Gly	Glu	Thr	Phe	Thr	290	295	300	
Cys	Thr	Ala	Ala	His	Pro	Glu	Leu	Lys	Thr	Pro	Leu	Thr	Ala	Asn	Ile	305	310	315	320
Thr	Lys	Ser	Gly	Asn	Thr	Phe	Arg	Pro	Glu	Val	His	Leu	Leu	Pro	Pro	325	330	335	
Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn	Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu	340	345	350	
Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp	Val	Leu	Val	Arg	Trp	Leu	Gln	Gly	355	360	365	
Ser	Gln	Glu	Leu	Pro	Arg	Glu	Lys	Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln	370	375	380	
Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr	Tyr	Ala	Val	Thr	Ser	Ile	Leu	Arg	385	390	395	400
Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys	Gly	Glu	Thr	Phe	Ser	Cys	Met	Val	405	410	415	

Gly	His	Glu	Ala	Leu	Pro	Leu	Ala	Phe	Thr	Gln	Lys	Thr	Ile	Asp	Arg	420	425	430	
Leu	Ala	Gly	Lys	Pro	Thr	His	Ile	Asn	Val	Ser	Val	Val	Met	Ala	Glu	435	440	445	
Ala	Asp	Gly	Thr	Cys	Tyr	Arg	Met	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	450	455	460	
Ala	Ile	Met	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Ile	Thr	Cys	Ser	465	470	475	480
Ala	Ser	Ser	Met	Val	Ser	Tyr	Met	His	Trp	Phe	Gln	Gln	Lys	Pro	Gly	485	490	495	
Thr	Ser	Pro	Lys	Leu	Trp	Leu	Tyr	Ser	Thr	Ser	Asn	Leu	Ala	Ser	Gly	500	505	510	
Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	515	520	525	
Thr	Ile	Ser	Arg	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	His	530	535	540	
Gln	Arg	Thr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	545	550	555	560
Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	565	570	575	
Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	580	585	590	
Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	595	600	605	
Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	610	615	620	
Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	625	630	635	640
Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	645	650	655	
Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				660	665		

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<212> DNA

<213> Artificial Sequence

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<210> 4
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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Met Gln Thr Ser Val
1 5

<210> 6
<211> 4
<212> PRT
<213> Artificial Sequence

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peptide

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